Amendments to the Specification:

Please replace the title at the top of pages 1 and 74 (Abstract page) with the following amended title:

METHODS FOR ELIMINATING ~~**FALSE DATA**~~ **INDISTINGUISHABLE AND FALSE DIFFERENTIALS** FROM COMPARATIVE DATA MATRICES ~~**AND FOR QUANTIFYING DATA MATRIX QUALITY**~~

Please replace paragraph [0039] with the following amended paragraph:

[0039] **Figure 4** shows a linear correlation between serial dilution of starting total RNA and the threshold cycles as measured by one-step hot-start real time RT-PCR for G3PDH using ~~**SYBR**~~ **SYBR®** green. The value of a threshold cycle is computed as the maximum of the second differential of a growth curve. The melting points range from 84.38 to 84.78.

Please replace paragraph [0047] with the following amended paragraph:

[0047] The specific gene expression profiling system described herein used a 1.7 K microarray chip of genes (i.e. a chip containing 2 x 1740 genes = 3480 genes) obtained commercially from the Ontario Cancer Institute. The samples are normal human brain tissue and meningiomas. The samples were labeled with the fluorescent labels Cy3™ and Cy5™ and hybridized to the genes on the slide. Images were obtained by inducing the labels to fluoresce by illuminating them within laser light of a suitable wavelength and imaging the fluorescence signals to produce a matrix of spots. Two measurements were made from each spot: 1) total intensity within the spot; and 2) local background intensity within a small rim surrounding the spot. Background-substrated intensities were calculated by subtracting the background measurements from the total intensity measurements.

Please replace paragraph [0082] with the following amended paragraph:

[0082] Titrated amounts of normal brain total RNA (configured as standard) and tumor total RNA samples (0.5 or 0.02 μg configured as unknown, Cepheid software) were assayed with

each primer pair using ~~SYBR~~ **SYBR®** green. Threshold cycles were computed as the maximum of the second differentials, and plotted against the log10 of the mass of normal brain total RNA. The plotted data fit linear curves whose equations permit computing the mass of normal brain RNA equivalent to 0.5 μg (or 0.02) of tumor RNA for a specific gene. The plotted data are shown in Fig. 4. Expression ratios normalized to G3PDH are:

$$\frac{\text{Computed mass of normal brain RNA for gene X}}{\text{Computed mass of normal brain RNA for G3PDH.}} \quad (6.1)$$

Please replace paragraph [0090] with the following amended paragraph:

[0090] Information on the antibodies used may be obtained from the ~~corresponding~~ web sites **of the various suppliers**. Anti-beta-catenin were purchased from Upstate biotech, 300 5th Avenue, 6th Floor, Waltham, MA 02451. Anti-glyceraldehyde**[[s]]**-3-phosphate dehydrogenase (G3PDH)~~, www.trevigen.com~~ **was purchased from Trevigen, Inc.** Anti-Akt, anti- phospho-Akt (Ser473), anti-p44/42 MAP kinase (ERK), and anti-phospho-p44/p42 Map Kinase (Thr202/tyr204, ERK-P) were purchased from Cell Signaling Technology, Inc, 166B Cummings Center, Beverly, MA 01915.

Please replace paragraph [0092] with the following amended paragraph:

[0092] All total RNA samples were analyzed in reference to a single standard obtained by pooling RNA from human occipital lobes. The latter were harvested and pooled from 4 individuals with no known neurological disease whose brains were frozen less than 3 hours postmortem. Total RNA (5-10 μg) was reverse transcribed and the cDNA products labeled by the amino-allyl method and hybridized to 19K gene microarrays purchased from the Ontario Cancer Institute. Each 19K microarray consisted of 2 slides containing a total of 38400 spots representing 19200 genes laid in duplicates (19200 spots/slide). The 19K microarray slides were scanned at 10 μm by a confocal scanner (Packard 4000XL scanner, Packard Bioscience; Meriden CT). Images were analyzed by the ~~Imagene~~ **Imagene®** Software (Biodiscovery; Los Angeles, CA).